

SEQUENCE LISTING

<110> Novo Nordisk A/S

<120> Novel Proteases And Variants Thereof

<130> 5665.204-WO

<140>

<141>

<150> PA 1999 01212

<151> 1999-08-31

<150> PA 1999 01500

<151> 1999-10-20

<160> 45

<170> PatentIn Ver. 2.1

<210> 1

<211> 948

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (1)..(948)

<220>

<221> mat_peptide

<222> (283)..(948)

<220>

<221> sig_peptide

<222> (1)..(93)

<223> pro_peptide (94) ... (282)

<400> 1

ttg gtt agt aaa aag agt gtt aaa cga ggt ttg atc aca ggt ctc att 48
Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu Ile Thr Gly Leu Ile
-90 -85 -80

ggt att tct att tat tct tta ggt atg cac ccg gcc caa gcc gcg cca 96
Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro
-75 -70 -65

tcg cct cat act cct gtt tca agc gat cct tca tac aaa gcg gaa aca 144
Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr
-60 -55 -50

tcg gtt act tat gac cca cac att aag agc gat caa tac ggc ttg tat 192
Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
-45 -40 -35

tca aaa gcg ttt aca ggc acc ggc aaa gtg aat gaa aca aag gaa aaa 240
Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Ash Glu Thr Lys Glu Lys
-30 -25 -20 -15

gcg gaa aaa aag tca ccc gcc aaa gct cct tac agc att aaa tcg gtg 288
Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val
-10 -5 -1 1

Kut B1

att ggt tct gat gat cgg aca agg gtc acc aac aca acc gca tat ccg 336
Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Ala Tyr Pro
5 10 15

tac aga gcg atc gtt cat att tca agc agc atc ggt tca tgc acc gga 384
Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
20 25 30

tgg atg atc ggt ccg aaa acc gtc gca aca gcc gga cac tgc atc tat 432
Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
35 40 45 50

gac aca tca agc ggt tca ttt gcc ggt aca gcc act gtt tcg ccg gga 480
Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
55 60 65

ccg aac ggg aca agc tat cct tac ggc tca gtt aaa tcg acg ccg tac 528
Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
70 75 80

ttt att ccg tca gga tgg aga agc gga aac acc aat tac gat tac gga 576
Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
85 90 95

gca atc gaa cta agc gaa ccg atc ggc aat act gtc gga tac ttc gga 624
Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
100 105 110

tac tcg tac act act tca tca ctt gtt ggg aca act gtt acc atc agc 672
Tyr Ser Tyr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
115 120 125 130

ggc tac cca ggc gat aaa aca gca ggc aca caa tgg cag cat tca gga 720
Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
135 140 145

ccg att gcc atc tcc gaa acg tat aaa ttg cag tac gca atg gac acg 768
Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
150 155 160

tac gga gga caa agc ggt tca ccg gta ttc gaa caa agc agc tcc aga 816
Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
165 170 175

acg aac tgt agc ggt ccg tgc tcg ctt gcc gta cac aca aat gga gta 864
Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
180 185 190

tac ggc ggc tcc tcg tac aac aga ggc acc ccg att aca aaa gag gtg 912
Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val
195 200 205 210

ttc gac aat ttg acc aac tgg aaa aac agc gca caa 948
Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
215 220

<210> 2
<211> 316
<212> PRT
<213> Bacillus licheniformis

<400> 2
Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu Ile Thr Gly Leu Ile
-90 -85 -80

Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro
 -75 -70 -65

Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr
 -60 -55 -50

Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
 -45 -40 -35

Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys
 -30 -25 -20 -15

Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val
 -10 -5 -1 1

Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro
 5 10 15

Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
 20 25 30

Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
 35 40 45 50

Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
 55 60 65

Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
 70 75 80

Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
 85 90 95

Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
 100 105 110

Tyr Ser Tyr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
 115 120 125 130

Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
 135 140 145

Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
 150 155 160

Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
 165 170 175

Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
 180 185 190

Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val
 195 200 205 210

Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
 215 220

<210> 3
 <211> 1026
 <212> DNA
 <213> Bacillus halmapalus AA513

<220>

1...-P1
 <221> CDS
 <222> (1)...(1026)
 <220>
 <221> mat_peptide
 <222> (361)...(1026)
 <220>
 <221> sig_peptide
 <222> (1)...(78)
 <223> Pro-peptide (79) ... (360)
 <400> 3
 atg aaa cta cta tta aaa ctt act ttt gta tgc ata ttt atg tta agt 48
 Met Lys Leu Leu Leu Lys Leu Thr Phe Val Cys Ile Phe Met Leu Ser
 -120 -115 -110 -105
 ggg att cta tcc cca gta aac gca act caa gct gag act ctt act aaa 96
 Gly Ile Leu Ser Pro Val Asn Ala Thr Gln Ala Glu Thr Leu Thr Lys
 -100 -95 -90
 tta aat aaa ata agt cag aag cag gaa cca tca tat aaa cta gat gaa 144
 Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp Glu
 -85 -80 -75
 gaa atg gat tat gtt cta att gat ttg gaa aca caa tct gaa tcg att 192
 Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser Ile
 -70 -65 -60
 att tcg ata gga gat aat acc gat ttg gga gat caa tcg ttt act tct 240
 Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr Ser
 -55 -50 -45
 tta ggg aag gtg gga cat gga gaa ctt gag aaa att aac tta gaa gaa 288
 Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu Glu
 -40 -35 -30 -25
 ttt cgt aat cct aat tta aca gta gta gac ccg tta aca cgt aag cct 336
 Phe Arg Asn Pro Asn Leu Thr Val Val Asp Pro Leu Thr Arg Lys Pro
 -20 -15 -10
 att gaa caa aaa atc agc cct ttt gtt gtt ata ggc gat gat ggg aga 384
 Ile Glu Gln Lys Ile Ser Pro Phe Val Val Ile Gly Asp Asp Gly Arg
 -5 -1 1 5
 aga caa gtt caa aat act tct ttc atg cca ttt cgt gca ctt act tat 432
 Arg Gln Val Gln Asn Thr Ser Phe Met Pro Phe Arg Ala Leu Thr Tyr
 10 15 20
 att gag ttt gga aac ctt aca agt aca tgg agt tgt tct gga ggt gtg 480
 Ile Glu Phe Gly Asn Leu Thr Ser Thr Trp Ser Cys Ser Gly Gly Val
 25 30 35 40
 att gga aca gat tta gtt gtt act aat gca cat tgt gta gaa ggt tct 528
 Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly Ser
 45 50 55
 gtg tta gca ggt act gta gtt cct ggt atg aac aat agt cag tgg gca 576
 Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp Ala
 60 65 70
 tat ggg cat tat agg gtt act cag att atc tac cct gat caa tac aga 624
 Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr Arg
 75 80 85
 aat aac ggt gct tca gag ttt gat tat gct ata ctt aga gta gca cct 672

Rub 21

Asn Asn Gly Ala Ser Glu Phe Asp Tyr Ala Ile Leu Arg Val Ala Pro
90 95 100

gac tct gat gga cgt cat att gga aac aga gct gga att tta tct ttt 720
Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser Phe
105 110 115 120

aca gaa aca gga act gtt aac gaa aat act ttt cta aga acg tat gga 768
Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr Gly
125 130 135

tac ccc ggt gat aaa ata tca gag aca aaa tta att tct ttg tgg gga 816
Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp Gly
140 145 150

atg gtt ggt cga tct gat gca ttt ttg cat cga gac cta ctg ttc tac 864
Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe Tyr
155 160 165

aat atg gac acc tat ttt ggt caa tca ggt tct cct gta tta aac agc 912
Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn Ser
170 175 180

gta gat tca atg gtt gcg gtt cat aat gca ggg tat atc gtt ggt ggt 960
Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly Gly
185 190 195 200

aat agg gaa att aat ggt ggt cct aaa atc aga aga gat ttt aca aac 1008
Asn Arg Glu Ile Asn Gly Gly Pro Lys Ile Arg Arg Asp Phe Thr Asn
205 210 215

tta ttt aat caa atg aac 1026
Leu Phe Asn Gln Met Asn
220

<210> 4
<211> 342
<212> PRT
<213> Bacillus halmapalus AA513

<400> 4
Met Lys Leu Leu Leu Lys Leu Thr Phe Val Cys Ile Phe Met Leu Ser
-120 -115 -110 -105

Gly Ile Leu Ser Pro Val Asn Ala Thr Gln Ala Glu Thr Leu Thr Lys
-100 -95 -90

Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp Glu
-85 -80 -75

Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser Ile
-70 -65 -60

Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr Ser
-55 -50 -45

Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu Glu
-40 -35 -30 -25

Phe Arg Asn Pro Asn Leu Thr Val Val Asp Pro Leu Thr Arg Lys Pro
-20 -15 -10

Ile Glu Gln Lys Ile Ser Pro Phe Val Val Ile Gly Asp Asp Gly Arg
-5 -1 1 5

Arg Gln Val Gln Asn Thr Ser Phe Met Pro Phe Arg Ala Leu Thr Tyr
 10 15 20

Ile Glu Phe Gly Asn Leu Thr Ser Thr Trp Ser Cys Ser Gly Gly Val
 25 30 35 40

Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly Ser
 45 50 55

Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp Ala
 60 65 70

Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr Arg
 75 80 85

Asn Asn Gly Ala Ser Glu Phe Asp Tyr Ala Ile Leu Arg Val Ala Pro
 90 95 100

Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser Phe
 105 110 115 120

Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr Gly
 125 130 135

Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp Gly
 140 145 150

Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe Tyr
 155 160 165

Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn Ser
 170 175 180

Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly Gly
 185 190 195 200

Asn Arg Glu Ile Asn Gly Gly Pro Lys Ile Arg Arg Asp Phe Thr Asn
 205 210 215

Leu Phe Asn Gln Met Asn
 220

<210> 5
 <211> 942
 <212> DNA
 <213> Bacillus licheniformis AC116

<220>
 <221> CDS
 <222> (1)..(942)

<220>
 <221> mat_peptide
 <222> (277)..(942)

<220>
 <221> sig_peptide
 <222> (1)..(87)
 <223> pro-peptide (88) ... (276)

<400> 5
 atg gcg aaa aat ggt gtt tca cgc gtt ttc att gcc gga ctc atc gga
 Met Ala Lys Asn Gly Val Ser Arg Val Phe Ile Ala Gly Leu Ile Gly
 -90 -85 -80

att tct att ttt tct tcg ggc att tac tct gca caa gct gca tca tcg 96
 Ile Ser Ile Phe Ser Ser Gly Ile Tyr Ser Ala Gln Ala Ala Ser Ser
 -75 -70 -65

ccg cat acc cca gtc tcc agc gac cct tcg tac aag ccc ggc tcc acc 144
 Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Gly Ser Thr
 -60 -55 -50 -45

tat gat ccc aac ata aaa att gac aat aac ggc gca tat tcg aaa gcc 192
 Tyr Asp Pro Asn Ile Lys Ile Asp Asn Asn Gly Ala Tyr Ser Lys Ala
 -40 -35 -30

ttc gaa gga acc gga aca ccc ggc ggc tcc gtt cag gcc aaa ccg aaa 240
 Phe Glu Gly Thr Gly Thr Pro Gly Gly Ser Val Gln Ala Lys Pro Lys
 -25 -20 -15

aaa gaa tcg ccc gcc ggc ccg cct tac agc cct aaa tcg gta atc ggc 288
 Lys Glu Ser Pro Ala Gly Pro Pro Tyr Ser Pro Lys Ser Val Ile Gly
 -10 -5 -1 1

tca gat gaa cgg aca agg gtg act gat aca acg gcc ttt cca tac aga 336
 Ser Asp Glu Arg Thr Arg Val Thr Asp Thr Ala Phe Pro Tyr Arg
 5 10 15 20

gca atc gtc cat att tca agc agc atc ggc tca tgc aca ggc tgg ctg 384
 Ala Ile Val His Ile Ser Ser Ile Gly Ser Cys Thr Gly Trp Leu
 25 30 35

atc gga ccg aaa acg gta gca acg gcc ggg cac tgc gtc tat gac acg 432
 Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Val Tyr Asp Thr
 40 45 50

gca agc cga tca ttc gcg gga acc gcc acc gtt tcc ccg gga cga aac 480
 Ala Ser Arg Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly Arg Asn
 55 60 65

ggt tca gct tac cct tac gga tct gtt aca tcg acc cgc tat ttc atc 528
 Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser Thr Arg Tyr Phe Ile
 70 75 80

ccg tcg ggt tgg cag agc gga aat tcc aat tat gac tac gca gcg atc 576
 Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr Asp Tyr Ala Ala Ile
 85 90 95 100

gag ctc agc cag ccg atc ggc aat acc gtc gga tat ttc gga tat tca 624
 Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr Ser
 105 110 115

tac acc gct tca tcg ctt gca gga gca ggc gtg acc atc agc gga tat 672
 Tyr Thr Ala Ser Ser Leu Ala Gly Ala Gly Val Thr Ile Ser Gly Tyr
 120 125 130

cca gga gac aaa aca aca ggc acc cag tgg caa atg tcc gga acg atc 720
 Pro Gly Asp Lys Thr Thr Gly Thr Gln Trp Gln Met Ser Gly Thr Ile
 135 140 145

gct gtt tca gaa acg tat aaa ctg caa tat gcg atc gac aca tac gga 768
 Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile Asp Thr Tyr Gly
 150 155 160

ggt caa agc ggt tcc ccg gta tat gag aaa agc agt tca agg aca aac 816
 Gly Gln Ser Gly Ser Pro Val Tyr Glu Lys Ser Ser Arg Thr Asn
 165 170 175 180

tgc agc ggc cca tgc tcg ctg gcc gtt cat acg aac ggc gtg tac gga 864

DNA B1

Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val Tyr Gly
185 190 195

gga tcc tct tac aac aga ggc acc cgc att acg aaa gaa gta ttt gat 912
Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val Phe Asp
200 205 210

aat ttc aca agc tgg aaa aac agc gca cag 942
Asn Phe Thr Ser Trp Lys Asn Ser Ala Gln
215 220

<210> 6

<211> 314

<212> PRT

<213> *Bacillus licheniformis* AC116

<400> 6

Met Ala Lys Asn Gly Val Ser Arg Val Phe Ile Ala Gly Leu Ile Gly
-90 -85 -80

Ile Ser Ile Phe Ser Ser Gly Ile Tyr Ser Ala Gln Ala Ala Ser Ser
-75 -70 -65

Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Gly Ser Thr
-60 -55 -50 -45

Tyr Asp Pro Asn Ile Lys Ile Asp Asn Asn Gly Ala Tyr Ser Lys Ala
-40 -35 -30

Phe Glu Gly Thr Gly Thr Pro Gly Gly Ser Val Gln Ala Lys Pro Lys
-25 -20 -15

Lys Glu Ser Pro Ala Gly Pro Pro Tyr Ser Pro Lys Ser Val Ile Gly
-10 -5 -1 1

Ser Asp Glu Arg Thr Arg Val Thr Asp Thr Thr Ala Phe Pro Tyr Arg
5 10 15 20

Ala Ile Val His Ile Ser Ser Ile Gly Ser Cys Thr Gly Trp Leu
25 30 35

Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Val Tyr Asp Thr
40 45 50

Ala Ser Arg Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly Arg Asn
55 60 65

Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser Thr Arg Tyr Phe Ile
70 75 80

Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr Asp Tyr Ala Ala Ile
85 90 95 100

Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr Ser
105 110 115

Tyr Thr Ala Ser Ser Leu Ala Gly Ala Gly Val Thr Ile Ser Gly Tyr
120 125 130

Pro Gly Asp Lys Thr Thr Gly Thr Gln Trp Gln Met Ser Gly Thr Ile
135 140 145

Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile Asp Thr Tyr Gly
150 155 160

Dub 131

Gly Gln Ser Gly Ser Pro Val Tyr Glu Lys Ser Ser Ser Arg Thr Asn
165 170 175 180

Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val Tyr Gly
185 190 195

Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val Phe Asp
200 205 210

Asn Phe Thr Ser Trp Lys Asn Ser Ala Gln
215 220

<210> 7
<211> 909
<212> DNA
<213> Bacillus pumilus BO32

<220>
<221> CDS
<222> (1)..(909)

<220>
<221> mat_peptide
<222> (265)..(909)

<220>
<221> sig_peptide
<222> (1)..(78)
<223> pro-peptide (79) ... (264)

<400> 7
atg atg aaa aag gtg aaa atg tta ctc cct tct cta ctt gtt ttt ggt 48
Met Met Lys Lys Val Lys Met Leu Leu Pro Ser Leu Leu Val Phe Gly
-85 -80 -75

gct tta agt gtg cct agt ttt gcc cat gcc gca tct gat tca gtg cta 96
Ala Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu
-70 -65 -60

acg tct gat tat gac atg gtg act tct gat gga aag gtg atc tct tca 144
Thr Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser
-55 -50 -45

agt gat ttc cac aat gat acg aaa tcc ccc tca tcc ttt gat aaa gtg 192
Ser Asp Phe His Asn Asp Thr Lys Ser Pro Ser Phe Asp Lys Val
-40 -35 -30 -25

gat gat cta tct tca act gtt ggt gaa aaa gta aaa cca cta tca aaa 240
Asp Asp Leu Ser Ser Thr Val Gly Glu Lys Val Lys Pro Leu Ser Lys
-20 -15 -10

tat tta aaa gac ttt caa aca aaa gtc gtc att gga gac gat ggt aga 288
Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg
-5 -1 1 5

aca aaa gta gca aat aca aga gtg gca cca tat aat tca att gct tat 336
Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr
10 15 20

act acg ttt ggc ggc tcc agc tgc acg ggg acc ctg att gcc cct aac 384
Thr Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn
25 30 35 40

aaa att ttg aca aac gga cac tgc gtg tac aat aca gca tcc aga agt 432

Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser
 45 50 55

tat	agt	gca	aaa	gga	tcg	gtg	tat	cca	ggc	atg	aat	gat	agt	act	gct		480
Tyr	Ser	Ala	Lys	Gly	Ser	Val	Tyr	Pro	Gly	Met	Asn	Asp	Ser	Thr	Ala		
			60				65						70				

gtg	aat	ggc	tca	gca	aat	atg	aca	gag	ttc	tat	gta	cca	agc	ggg	tat		528
Val	Asn	Gly	Ser	Ala	Asn	Met	Thr	Glu	Phe	Tyr	Val	Pro	Ser	Gly	Tyr		
			75			80					85						

atc	aat	aca	ggt	gct	agc	caa	tat	gat	ttt	gcc	gtg	atc	aaa	aca	gat		576
Ile	Asn	Thr	Gly	Ala	Ser	Gln	Tyr	Asp	Phe	Ala	Val	Ile	Lys	Thr	Asp		
			90			95					100						

acq	aac	att	ggc	aat	aca	gtt	ggt	tac	cgt	tcc	atc	cgt	cag	gtg	aca		624
Thr	Asn	Ile	Gly	Asn	Thr	Val	Gly	Tyr	Arg	Ser	Ile	Arg	Gln	Val	Thr		
			105			110				115				120			

aac	tta	act	ggg	aca	acg	att	aaa	att	tct	gga	tat	cca	ggt	gat	aaa		672
Asn	Leu	Thr	Gly	Thr	Thr	Ile	Lys	Ile	Ser	Gly	Tyr	Pro	Gly	Asp	Lys		
			125					130				135					

atg	aga	tca	act	ggc	aag	atc	tcg	cag	tgg	gag	atg	tca	ggt	cct	gtg		720
Met	Arg	Ser	Thr	Gly	Lys	Ile	Ser	Gln	Trp	Glu	Met	Ser	Gly	Pro	Val		
			140				145				150						

aca	aga	gaa	gat	acg	aat	ctc	gca	tac	tat	atg	att	gat	aca	ttt	agt		768
Thr	Arg	Glu	Asp	Thr	Asn	Leu	Ala	Tyr	Tyr	Met	Ile	Asp	Thr	Phe	Ser		
			155				160				165						

gga	aat	tca	ggc	tca	gct	atg	cta	gat	caa	aat	cag	caa	att	gtt	ggg		816
Gly	Asn	Ser	Gly	Ser	Ala	Met	Leu	Asp	Gln	Asn	Gln	Gln	Ile	Val	Gly		
			170				175				180						

gtt	cat	aac	gca	ggg	tat	tca	aac	ggt	acg	att	aat	ggc	ggt	cca	aaa		864
Val	His	Asn	Ala	Gly	Tyr	Ser	Asn	Gly	Thr	Ile	Asn	Gly	Gly	Pro	Lys		
			185			190				195				200			

gcg	aca	gct	gcc	ttt	gtt	gaa	ttt	atc	aac	tat	gca	aaa	gct	caa			909
Ala	Thr	Ala	Ala	Phe	Val	Glu	Phe	Ile	Asn	Tyr	Ala	Lys	Ala	Gin			
				205				210				215					

<210> 8
 <211> 303
 <212> PRT
 <213> Bacillus pumilus BO32

<400> 8
 Met Met Lys Lys Val Lys Met Leu Leu Pro Ser Leu Leu Val Phe Gly
 -85 -80 -75

Ala	Leu	Ser	Val	Pro	Ser	Phe	Ala	His	Ala	Ala	Ser	Asp	Ser	Val	Leu	
							-70				-65			-60		

Thr	Ser	Asp	Tyr	Asp	Met	Val	Thr	Ser	Asp	Gly	Lys	Val	Ile	Ser	Ser	
							-55				-45					

Ser	Asp	Phe	His	Asn	Asp	Thr	Lys	Ser	Pro	Ser	Ser	Phe	Asp	Lys	Val	
							-40			-30			-25			

Asp	Asp	Leu	Ser	Ser	Thr	Val	Gly	Glu	Lys	Val	Lys	Pro	Leu	Ser	Lys	
							-20			-15			-10			

Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg

Dut-B1

-5 -1 1 5

Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr
10 15 20

Thr Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn
25 30 35 40

Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser
45 50 55

Tyr Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala
60 65 70

Val Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr
75 80 85

Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp
90 95 100

Thr Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr
105 110 115 120

Asn Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys
125 130 135

Met Arg Ser Thr Gly Lys Ile Ser Gln Trp Glu Met Ser Gly Pro Val
140 145 150

Thr Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Met Ile Asp Thr Phe Ser
155 160 165

Gly Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly
170 175 180

Val His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys
185 190 195 200

Ala Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln
205 210 215

<210> 9
<211> 954
<212> DNA
<213> Bacillus licheniformis CDJ31

<220>
<221> CDS
<222> (1)..(954)

<220>
<221> mat_peptide
<222> (289)..(954)

<220>
<221> sig_peptide
<222> (1)..(84)
<223> pro-peptide (85) ... (288)

<400> 9
atg aaa aaa agt gtg aca cgc gta tta atg gcc ggt ctt att gga ata 48
Met Lys Lys Ser Val Thr Arg Val Leu Met Ala Gly Leu Ile Gly Ile
-95 -90 -85

LB-B1

tct att tat tct atg ggc atc gac tcc gct caa gct gca tca tcg ccg 96
Ser Ile Tyr Ser Met Gly Ile Asp Ser Ala Gln Ala Ala Ser Ser Pro
-80 -75 -70 -65

cat act cct gtc tct agc gat cct tca tac aag ccc gac tca tcc gca 144
His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Asp Ser Ser Ala
-60 -55 -50

agc tat gat cct gct att aaa acc aac aaa aac ggc gcc tat tca aaa 192
Ser Tyr Asp Pro Ala Ile Lys Thr Asn Lys Asn Gly Ala Tyr Ser Lys
-45 -40 -35

gca ttt gaa ggt aca gga aaa cta gac gct ccc ctt tat cag gaa aaa 240
Ala Phe Glu Gly Thr Gly Lys Leu Asp Ala Pro Leu Tyr Gln Glu Lys
-30 -25 -20

agc aaa cca acc aaa aaa tcc cct gcc gga cca cgt tac agc ccc aaa 288
Ser Lys Pro Thr Lys Lys Ser Pro Ala Gly Pro Arg Tyr Ser Pro Lys
-15 -10 -5 -1

tcc gtg att ggt tct gat gaa cgg acg aga gtg aca aac act acc gca 336
Ser Val Ile Gly Ser Asp Glu Arg Thr Arg Val Thr Asn Thr Thr Ala
1 5 10 15

tat cca tac aga gcg atc gtg cat att tca agc agc atc ggg tct tgc 384
Tyr Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys
20 25 30

acc ggc tcc ctg atc ggt ccg aaa acg gtg gca acg gcc gga cac tgc 432
Thr Gly Ser Leu Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys
35 40 45

att tat gac aca gcg agc ggg tca ttc gcc gga acc gct acc gtt tct 480
Ile Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser
50 55 60

ccg gga cgg aac ggt tca aca tat ccg tac gga tca gtt aca tca acc 528
Pro Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser Thr
65 70 75 80

cgc tat ttc atc ccg tca ggc tat cga agc gga aat tcg aat tac gac 576
Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr Asp
85 90 95

tac gga gcc ata gag ctc agc cag ccg atc ggc aac acc gtc ggg tat 624
Tyr Gly Ala Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr
100 105 110

ttc gga tat tcc tac acc acc tcg tct ctc gtt ggg tca agc gtt acc 672
Phe Gly Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Ser Ser Val Thr
115 120 125

atc atc gga tat cca ggc gac aaa aca tcg ggc acc caa tgg cag atg 720
Ile Ile Gly Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met
130 135 140

tcc gga aat atc gcc gtc tca gaa aca tat aaa ctg caa tat gcg atc 768
Ser Gly Asn Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile
145 150 155 160

gac aca tac gga ggg cag agc ggc tct ccc gta tat gag gcg agc agc 816
Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Tyr Glu Ala Ser Ser
165 170 175

tcc aga acg aat tgc agc ggc cca tgt tcg ctg gcc gtt cat acg aat 864
Ser Arg Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn

KwB(3)

180 185 190
ggg gtg tac gga gga tct tca tac aac aga ggc acc cgg att aca aaa 912
Gly Val Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys
195 200 205
gaa gta ttc gat aat ttg aca aac tgg aaa aac agc gcc caa 954
Glu Val Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
210 215 220

<210> 10
<211> 318
<212> PRT
<213> Bacillus licheniformis CDJ31

<400> 10
Met Lys Ser Val Thr Arg Val Leu Met Ala Gly Leu Ile Gly Ile -95 -90 -85
Ser Ile Tyr Ser Met Gly Ile Asp Ser Ala Gln Ala Ala Ser Ser Pro -80 -75 -70 -65
His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Asp Ser Ser Ala -60 -55 -50
Ser Tyr Asp Pro Ala Ile Lys Thr Asn Lys Asn Gly Ala Tyr Ser Lys -45 -40 -35
Ala Phe Glu Gly Thr Gly Lys Leu Asp Ala Pro Leu Tyr Gln Glu Lys -30 -25 -20
Ser Lys Pro Thr Lys Lys Ser Pro Ala Gly Pro Arg Tyr Ser Pro Lys -15 -10 -5 -1
Ser Val Ile Gly Ser Asp Glu Arg Thr Arg Val Thr Asn Thr Thr Ala 1 5 10 15
Tyr Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ile Gly Ser Cys 20 25 30
Thr Gly Ser Leu Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys 35 40 45
Ile Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser 50 55 60
Pro Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser Thr 65 70 75 80
Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr Asp 85 90 95
Tyr Gly Ala Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr 100 105 110
Phe Gly Tyr Ser Tyr Thr Ser Ser Leu Val Gly Ser Ser Val Thr 115 120 125
Ile Ile Gly Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met 130 135 140
Ser Gly Asn Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile 145 150 155 160
Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Tyr Glu Ala Ser Ser

Det 1

165 170 175
Ser Arg Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn
180 185 190
Gly Val Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys
195 200 205
Glu Val Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
210 215 220

<210> 11
<211> 906
<212> DNA
<213> *Bacillus pumilus* JA96

<220>
<221> CDS
<222> (1)...(906)

<220>
<221> mat_peptide
<222> (262)...(906)

<220>
<221> sig_peptide
<222> (1)...(75)
<223> pro-peptide (76) ... (261)

<400> 11
atg aaa aag gtg aaa aaa tta atc cct tct cta ctc gtt ttt ggt gct 48
Met Lys Lys Val Lys Lys Leu Ile Pro Ser Leu Leu Val Phe Gly Ala
-85 -80 -75

tta agt gtg cct agt ttt gcc cat gca gca tct gat tca gta ctt acg 96
Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu Thr
-70 -65 -60

tct gat tat gac atg gtg act tct gac gga aag gtg att tct tca gct 144
Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser Ala
-55 -50 -45 -40

gac ttc cac aac gat atg aaa acc ccc tca tcc ttt gac aaa gtg gat 192
Asp Phe His Asn Asp Met Lys Thr Pro Ser Ser Phe Asp Lys Val Asp
-35 -30 -25

gat ctc tct act att ggc gaa aaa gta aaa cca ctc aca aca tat 240
Asp Leu Ser Ser Thr Ile Gly Glu Lys Val Lys Pro Leu Thr Thr Tyr
-20 -15 -10

tta aaa gac ttt caa aca aaa gta gtc att gga gac gat ggt aga aca 288
Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg Thr
-5 -1 1 5

aaa gtg acg aat aca aga gta gca ccc tat aat tct att gct tat att 336
Lys Val Thr Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr Ile
10 15 20 25

aca ttt ggt gga tct agc tgc act gga aca ctc att gct cca aac aaa 384
Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn Lys
30 35 40

ata ttg aca aac gga cac tgc gtc tac aat aca gcc aca aga agt tat 432
Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Thr Arg Ser Tyr

Ruth B

45 50 55

aat gca aaa ggg tct gtc tac cca ggc atg aat gac agc acg gct gtg 480
Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala Val
60 65 70

aac ggc tca gca aac atg acc gaa ttc tat gta cca agc gga tat atc 528
Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr Ile
75 80 85

aac acg ggg gcg aat caa tat gat ttt gcc gtc att aaa aca gat acg 576
Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp Thr
90 95 100 105

aac att gga aat acg gtc ggc tat cgc tct att cgt caa gtg aca aat 624
Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr Asn
110 115 120

cta aca ggt aca acg att aaa att tct gga tat cca ggt gat aaa atg 672
Leu Thr Gly Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys Met
125 130 135

aga tcg act ggc aaa gtg tca oaa tgg gaa atg tca ggt cca gtc acg 720
Arg Ser Thr Gly Lys Val Ser Gln Trp Glu Met Ser Gly Pro Val Thr
140 145 150

aga gaa gat acg aat ctc gca tac tat acg atc gat aca ttt acg gga 768
Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser Gly
155 160 165

aac tct ggc tct gcg atg cta gat cag aac caa caa atc gtc ggg gtc 816
Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly Val
170 175 180 185

cat aat gcg ggt tat tca aat gga acg atc aac ggt gga cca aaa gcg 864
His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys Ala
190 195 200

act gct gcc ttt gtt gaa ttt atc aac tat gcg aag gcg caa 906
Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln
205 210 215

<210> 12
<211> 302
<212> PRT
<213> *Bacillus pumilus JA96*

<400> 12
Met Lys Val Lys Lys Leu Ile Pro Ser Leu Leu Val Phe Gly Ala
-85 -80 -75

Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu Thr
-70 -65 -60

Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser Ala
-55 -50 -45 -40

Asp Phe His Asn Asp Met Lys Thr Pro Ser Ser Phe Asp Lys Val Asp
-35 -30 -25

Asp Leu Ser Ser Thr Ile Gly Glu Lys Val Lys Pro Leu Thr Thr Tyr
-20 -15 -10

Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg Thr
-5 -1 1 5

Bacillus

Lys Val Thr Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr Ile
10 15 20 25

Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn Lys
30 35 40

Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Thr Arg Ser Tyr
45 50 55

Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala Val
60 65 70

Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr Ile
75 80 85

Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp Thr
90 95 100 105

Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr Asn
110 115 120

Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys Met
125 130 135

Arg Ser Thr Gly Lys Val Ser Gln Trp Glu Met Ser Gly Pro Val Thr
140 145 150

Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser Gly
155 160 165

Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly Val
170 175 180 185

His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys Ala
190 195 200

Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln
205 210 215

<210> 13
<211> 939
<212> DNA
<213> *Bacillus subtilis* IS75

<220>
<221> CDS
<222> (1)..(939)

<220>
<221> mat_peptide
<222> (280)..(939)

<220>
<221> sig_peptide
<222> (1)..(102)
<223> pro-peptide (103) ... (279)

<400> 13
atg aaa tta gtt cca aga ttc aga aaa caa tgg ttc gct tac tta acg 48
Met Lys Leu Val Pro Arg Phe Arg Lys Gln Trp Phe Ala Tyr Leu Thr
-90 -85 -80

gtt ttg tgt ttg gct ttg gca gca gcg gtt tct ttt ggc gta ccg gca 96

Part 151

Val	Leu	Cys	Leu	Ala	Leu	Ala	Ala	Ala	Val	Ser	Phe	Gly	Val	Pro	Ala	
-75									-70							-65
aaa	gcg	gca	gag	aac	ccg	caa	act	tct	gta	tcg	aat	acc	ggt	aaa	gaa	144
Lys	Ala	Ala	Glu	Asn	Pro	Gln	Thr	Ser	Val	Ser	Asn	Thr	Gly	Lys	Glu	
-60								-55					-50			
gct	gat	gct	acg	aaa	aac	caa	acg	tca	aaa	gca	gat	cag	gtt	tcc	gcc	192
Ala	Asp	Ala	Thr	Lys	Asn	Gln	Thr	Ser	Lys	Ala	Asp	Gln	Val	Ser	Ala	
-45								-40					-35			-30
cct	tat	gag	gga	acc	gga	aaa	aca	agt	aaa	tcg	tta	tac	ggc	ggc	caa	240
Pro	Tyr	Glu	Gly	Thr	Gly	Lys	Thr	Ser	Lys	Ser	Leu	Tyr	Gly	Gly	Gln	
-25									-20						-15	
acg	gaa	ctg	gaa	aaa	aac	att	caa	acc	tta	cag	cct	tcg	agc	att	atc	288
Thr	Glu	Leu	Glu	Lys	Asn	Ile	Gln	Thr	Leu	Gln	Pro	Ser	Ser	Ile	Ile	
-10									-5				-1		1	
gga	act	gat	gaa	cgc	acc	aga	atc	tcc	agc	aca	tct	ttt	cca	tat		336
Gly	Thr	Asp	Glu	Arg	Thr	Arg	Ile	Ser	Ser	Thr	Thr	Ser	Phe	Pro	Tyr	
5								10					15			
aga	gca	acc	gtt	caa	ctg	tca	atc	aag	tat	ccc	aac	act	tca	agc	act	384
Arg	Ala	Thr	Val	Gln	Leu	Ser	Ile	Lys	Tyr	Pro	Asn	Thr	Ser	Ser	Thr	
20								25					30			35
tat	gga	tgt	acc	gga	ttt	tta	gtc	aat	cca	aat	aca	gtc	gtc	acg	gct	432
Tyr	Gly	Cys	Thr	Gly	Phe	Leu	Val	Asn	Pro	Asn	Thr	Val	Val	Thr	Ala	
40									45						50	
gga	cat	tgt	gtg	tac	agc	cag	gat	cat	gga	tgg	gct	tcg	acg	ata	acc	480
Gly	His	Cys	Val	Tyr	Ser	Gln	Asp	His	Gly	Trp	Ala	Ser	Thr	Ile	Thr	
55								60						65		
gcc	gcf	ccg	ggc	cgc	aat	ggt	tcg	tca	tat	ccg	tac	ggt	act	tat	tca	528
Ala	Ala	Pro	Gly	Arg	Asn	Gly	Ser	Ser	Tyr	Pro	Tyr	Gly	Thr	Tyr	Ser	
70								75						80		
ggc	acg	atg	ttt	tac	tcc	gtc	aaa	gga	tgg	acg	gaa	agc	aaa	gac	acc	576
Gly	Thr	Met	Phe	Tyr	Ser	Val	Lys	Gly	Trp	Thr	Glu	Ser	Lys	Asp	Thr	
85								90						95		
aac	tat	gat	tac	gga	gct	att	aaa	tta	aac	ggt	tct	cct	gga	aac	acg	624
Asn	Tyr	Asp	Tyr	Gly	Ala	Ile	Lys	Leu	Asn	Gly	Ser	Pro	Gly	Asn	Thr	
100								105						110		115
gtt	ggc	tgg	tac	ggc	tac	cgg	act	aca	aac	agc	agc	agt	ccc	gtg	ggc	672
Val	Gly	Trp	Tyr	Gly	Tyr	Arg	Thr	Asn	Ser	Ser	Ser	Pro	Val	Gly		
120								125						130		
ctt	tcc	tcg	tca	gtg	aca	gga	tcc	cca	tgt	gac	aaa	acc	ttt	ggc	acg	720
Leu	Ser	Ser	Val	Thr	Gly	Phe	Pro	Cys	Asp	Lys	Thr	Phe	Gly	Thr		
135								140						145		
atg	tgg	tct	gat	aca	aag	ccg	att	cgc	tcc	gct	gaa	acg	tat	aag	ctg	768
Met	Trp	Ser	Asp	Thr	Lys	Pro	Ile	Arg	Ser	Ala	Glu	Thr	Tyr	Lys	Leu	
150								155						160		
acc	tat	aca	acc	gat	acg	tac	ggc	tgc	caa	agc	ggc	tcg	cct	gtt	tat	816
Thr	Tyr	Thr	Asp	Thr	Tyr	Gly	Cys	Gln	Ser	Gly	Ser	Pro	Val	Tyr		
165								170						175		
cga	aac	tac	agt	gat	aca	ggg	cag	aca	gct	att	gcc	att	cac	acg	aac	864
Arg	Asn	Tyr	Ser	Asp	Thr	Gly	Gln	Thr	Ala	Ile	Ala	Ile	His	Thr	Asn	
180								185						190		195

12/21/81

gga gga tcg tca tat aac ttg gga aca agg gtg acg aac gat gta ttc 912
Gly Gly Ser Ser Tyr Asn Leu Gly Thr Arg Val Thr Asn Asp Val Phe
200 205 210

aac aat att caa tat tgg gca aat caa 939
Asn Asn Ile Gln Tyr Trp Ala Asn Gln
215 220

<210> 14
<211> 313
<212> PRT
<213> Bacillus subtilis IS75

<400> 14
Met Lys Leu Val Pro Arg Phe Arg Lys Gln Trp Phe Ala Tyr Leu Thr
-90 -85 -80

Val Leu Cys Leu Ala Leu Ala Ala Ala Val Ser Phe Gly Val Pro Ala
-75 -70 -65

Lys Ala Ala Glu Asn Pro Gln Thr Ser Val Ser Asn Thr Gly Lys Glu
-60 -55 -50

Ala Asp Ala Thr Lys Asn Gln Thr Ser Lys Ala Asp Gln Val Ser Ala
-45 -40 -35 -30

Pro Tyr Glu Gly Thr Gly Lys Thr Ser Lys Ser Leu Tyr Gly Gly Gln
-25 -20 -15

Thr Glu Leu Glu Lys Asn Ile Gln Thr Leu Gln Pro Ser Ser Ile Ile
-10 -5 -1 1

Gly Thr Asp Glu Arg Thr Arg Ile Ser Ser Thr Thr Ser Phe Pro Tyr
5 10 15

Arg Ala Thr Val Gln Leu Ser Ile Lys Tyr Pro Asn Thr Ser Ser Thr
20 25 30 35

Tyr Gly Cys Thr Gly Phe Leu Val Asn Pro Asn Thr Val Val Thr Ala
40 45 50

Gly His Cys Val Tyr Ser Gln Asp His Gly Trp Ala Ser Thr Ile Thr
55 60 65

Ala Ala Pro Gly Arg Asn Gly Ser Ser Tyr Pro Tyr Gly Thr Tyr Ser
70 75 80

Gly Thr Met Phe Tyr Ser Val Lys Gly Trp Thr Glu Ser Lys Asp Thr
85 90 95

Asn Tyr Asp Tyr Gly Ala Ile Lys Leu Asn Gly Ser Pro Gly Asn Thr
100 105 110 115

Val Gly Trp Tyr Gly Tyr Arg Thr Thr Asn Ser Ser Ser Pro Val Gly
120 125 130

Leu Ser Ser Ser Val Thr Gly Phe Pro Cys Asp Lys Thr Phe Gly Thr
135 140 145

Met Trp Ser Asp Thr Lys Pro Ile Arg Ser Ala Glu Thr Tyr Lys Leu
150 155 160

Thr Tyr Thr Thr Asp Thr Tyr Gly Cys Gln Ser Gly Ser Pro Val Tyr
165 170 175

Pext(B1)

Arg Asn Tyr Ser Asp Thr Gly Gln Thr Ala Ile Ala Ile His Thr Asn
180 185 190 195

Gly Gly Ser Ser Tyr Asn Leu Gly Thr Arg Val Thr Asn Asp Val Phe
200 205 210

Asn Asn Ile Gln Tyr Trp Ala Asn Gln
215 220

<210> 15
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Variation

<400> 15
Glu Lys Ala Ser
1

<210> 16
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Variation

<400> 16
Ser Glu Lys Ala Ser Thr
1 5

<210> 17
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Variation

<400> 17
Ser Glu Glu Thr
1

<210> 18
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1)...(38)
<223> n = A,T,C or G

<400> 18
ggatggagaa gcggaaacac naaytaygay tayggngc

<210> 19
<211> 10

38

DNA BY

<212> PRT
<213> Artificial Sequence

<220>
<223> Variation

<400> 19
Gly Trp Arg Ser Gly Asn Tyr Asp Tyr Gly
1 5 10

<210> 20
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> 12,15
<223> n = deoxyInosine

<221> misc_feature
<222> 18,21 24
<223> n = A,T,C or G

<400> 20
cccaagctt g tngynacngc nggncayt

28

<210> 21
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Variation

<221> VARIANT
<222> 2<223> Xaa = Ala or Val

<400> 21
Val Xaa Thr Ala Gly His
1 5

<210> 22
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1)...(36)
<223> n = A,T,C or G

<400> 22
gaataaccggt gaaccgcttt gncmncrta ngtrtc

36

<210> 23
<211> 12
<212> PRT
<213> Artificial Sequence

cut b1

<220>
<223> Variation

<221> VARIANT

<222> 5

<223> Xaa = Gly or Cys or Trp

<400> 23

Asp Thr Tyr Gly Xaa Gln Ser Gly Ser Pro Val Phe
1 5 10

<210> 24

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<221> misc_feature

<222> (1)...(26)

<223> n = A,T,C or G

<400> 24

gctcttagat ydatngcncc rtaartc

26

<210> 25

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Variation

<221> VARIANT

<222> 6

<223> Xaa = Glu or Lys

<400> 25

Asp Tyr Gly Ala Ile Xaa
1 5

<210> 26

<211> 143

<212> DNA

<213> Bacillus

<400> 26

gcgtctatga cacggcaagc cgatcattcg cgggaaccgc caccgttcc ccgggacgaa
acggttcagc ttacccttac ggatctgtta catcgaccc ctatttcatac ccgtcgggtt
ggcagagcgg aaattccaat tat

60

120

143

<210> 27

<211> 48

<212> PRT

<213> Bacillus

<400> 27

Cys Val Tyr Asp Thr Ala Ser Arg Ser Phe Ala Gly Thr Ala Thr Val
1 5 10 15
Ser Pro Gly Arg Asn Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser
20 25 30
Thr Arg Tyr Phe Ile Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr
35 40 45

Part (3)

<210> 28
<211> 184
<212> DNA
<213> Bacillus

<400> 28
gatcgagctc agccagccga tcggcaatac cgtcgatatt ttcggatatt catacaccgc
ttcatcgctt gcaggagcag gcgtgaccat cagcgatatt ccaggagaca aaacaacagg
cacccatgtgg caaatgtccg gaacgatcgc tgtttcagaa acgtataaac tgcaatatgc
gatc

60
120
180
184

<210> 29
<211> 61
<212> PRT
<213> Bacillus

<400> 29
Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr
1 5 10 15
Ser Tyr Thr Ala Ser Ser Leu Ala Gly Ala Gly Val Thr Ile Ser Gly
20 25 30
Tyr Pro Gly Asp Lys Thr Thr Gly Thr Gln Trp Gln Met Ser Gly Thr
35 40 45
Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile
50 55 60

<210> 30
<211> 143
<212> DNA
<213> Bacillus

<400> 30
gcatttatqa cacagcgagc qggtcattcg ccggAACCGC taccgtttct ccgggacgga
acggttcaac atatccgtac ggatcaggta catcaacccg ctatttcatac ccgtcaggct
atcgaagcgg aaattcgaat tac

60
120
143

<210> 31
<211> 48
<212> PRT
<213> Bacillus

<400> 31
Cys Ile Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val
1 5 10 15
Ser Pro Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser
20 25 30
Thr Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr
35 40 45

<210> 32
<211> 184
<212> DNA
<213> Bacillus

<400> 32
catagagctc agccagccga tcggcaaacac cgtcggtat ttccggatatt cctacaccac
ctcgctctc gttgggtcaa gcgttaccat catcgatatt ccaggcaca aaacatcggt
cacccatgtgg cagatgtccg gaaatatcgc cgtctcagaa acatataaac tgcaatatgc
gatc

60
120
180
184

<210> 33
<211> 61
<212> PRT
<213> Bacillus

120t 131

<400> 33
Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr
1 5 10 15
Ser Tyr Thr Thr Ser Ser Leu Val Gly Ser Ser Val Thr Ile Ile Gly
20 25 30
Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met Ser Gly Asn
35 40 45
Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile
50 55 60

<210> 34
<211> 19
<212> DNA
<213> Bacillus

<400> 34
cgtaagggtta agctgaacc

19

<210> 35
<211> 23
<212> DNA
<213> Bacillus

<400> 35
caggagacaa aacaacagca ggc

23

<210> 36
<211> 18
<212> DNA
<213> Bacillus

<400> 36
gtcccgagaa aacggtag

18

<210> 37
<211> 20
<212> DNA
<213> Bacillus

<400> 37
caccacctcg tcttcgttg

20

<210> 38
<211> 29
<212> DNA
<213> Bacillus

<220>
<221> misc_feature
<222> 18, 21
<223> Xaa = deoxyInosine

<221> misc_feature
<222> 27
<223> n = A, G, C or T

<400> 38
gctctagacg tyttrtcncm nggrwancc

29

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Variation

DnaV1

<221> VARIANT
<222> 2
<223> Xaa = is Tyr or Phe

<221> VARIANT
<222> 4
<223> Xaa = is Gly or Cys

<400> 39
Gly Xaa Pro Xaa Asp Lys Thr
1 5

<210> 40
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> 12,15,21
<223> n = is deoxyInosine

<400> 40
cccaagcttg tngtnathgg ngaygaygg

29

<210> 41
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Variation

<400> 41
Val Val Ile Gly Gly Asp Asp Gly
1 5

<210> 42
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 42
gcacggaccg ttgcagttcg ttctggagc

29

<210> 43<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 43
ccggcaaagt gaatgaaaca aaggaaaaag cg

33

<210> 44
<211> 31
<212> DNA

Part 1/2

<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature

<222> (1) ... (31)

<223> n = A, T, C or G

<400> 44

atgcaccgga tggnnhatag gtccgaaaac c

31

<210> 45

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 45

ccctttaacc gcacaggtt t

21